| | | | |
|---|---|---|---|
| VHL/E | 1 | ATGACACCGACGACGACGACCGCGGAACTCACG | 33 |
| VHL/E | 34 | ACGGAGTTTGACTACGACGATGAAGCGACTCCC | 66 |
| VHL/E | 67 | TGTGTCCTCACCGACGTGCTTAATCAGTCGAAG | 99 |
| VHL/E | 100 | CCAGTCACGTTGTTTCTGTACGGCGTTGTCTTT | 132 |
| VHL/E | 133 | CTCTTCGGTTCCATCGGCAACTTCTTGGTGATC | 165 |
| VHL/E | 166 | TTCACCATCACCTGGCGACGTCGGATTCAATGT | 198 |
| VHL/E | 199 | TCCGGCGATGTTTACTTTATCAACCTCGCGGCC | 231 |
| VHL/E | 232 | GCCGATTTGCTTTTCGTTTGTACACTACCTCTG | 264 |
| VHL/E | 265 | TGGATGCAATACCTCCTAGATCACAACTCCCTA | 297 |
| VHL/E | 298 | GCCAGCGTGCCGTGTACGTTACTCACTGCCTGT | 330 |
| VHL/E | 331 | TTCTACGTGGCTATGTTTGCCAGTTTGTGTTTT | 363 |
| VHL/E | 364 | ATCACGGAGATTGCACTCGATCGCTACTACGCT | 396 |
| VHL/E | 397 | ATTGTTTACATGAGATATCGGCCTGTAAAACAG | 429 |
| VHL/E | 430 | GCCTGCCTTTTCAGTATTTTTTGGTGGATCTTT | 462 |
| VHL/E | 463 | GCCGTGATCATCGCCATTCCACACTTTATGGTG | 495 |
| VHL/E | 496 | GTGACCAAAAAAGACAATCAATGTATGACCGAC | 528 |
| VHL/E | 529 | TACGACTACTTAGAGGTCAGTTACCCGATCATC | 561 |
| VHL/E | 562 | CTCAACGTAGAACTCATGCTCGGTGCTTTCGTG | 594 |
| VHL/E | 595 | ATCCCGCTCAGTGTCATCAGCTACTGCTACTAC | 627 |
| VHL/E | 628 | CGCATTTCCAGAATCGTTGCGGTGTCTCAGTCG | 660 |
| VHL/E | 661 | CGCCACAAAGGCCGCATTGTACGGGTACTTATA | 693 |
| VHL/E | 694 | GCGGTCGTGCTTGTCTTTATCATCTTTTGGCTG | 726 |
| VHL/E | 727 | CCGTACCACCTGACGCTGTTTGTGGACACGTTG | 759 |
| VHL/E | 760 | AAACTGCTCAAATGGATCTCCAGCAGCTGCGAG | 792 |
| VHL/E | 793 | TTCGAAAAATCACTCAAGCGCGCGCTCATCTTG | 825 |
| VHL/E | 826 | ACCGAGTCACTCGCCTTTTGTCACTGTTGTCTC | 858 |
| VHL/E | 859 | AATCCGCTGCTGTACGTCTTCGTGGGCACCAAG | 891 |
| VHL/E | 892 | TTTCGGCAAGAACTGCACTGTCTGCTGGCCGAG | 924 |
| VHL/E | 925 | TTTCGCCAGCGACTGTTTTCCCGCGATGTATCC | 957 |
| VHL/E | 958 | TGGTACCACAGCATGAGCTTTTCGCGTCGGAGC | 990 |
| VHL/E | 991 | TCGCCGAGCCGAAGAGAGACGTCTTCCGACACG | 1023 |
| VHL/E | 1024 | CTGTCCGACGAGGCGTGTCGCGTCTCACAAATT | 1056 |
| VHL/E | 1057 | ATACCGTAA | 1065 |

FIG. 1A

| | | | |
|---|---|---|---|
| VHL/E | 1 | MTPTTTTAELTTEFDYDDEATPCVLTDVLNQSK | 33 |
| VHL/E | 34 | PVTLFLYGVVFLFGSIGNFLVIFTITWRRRIQC | 66 |
| VHL/E | 67 | SGDVYFINLAAADLLFVCTLPLWMQYLLDHNSL | 99 |
| VHL/E | 100 | ASVPCTLLTACFYVAMFASLCFITEIALDRYYA | 132 |
| VHL/E | 133 | IVYMRYRPVKQACLFSIFWWIFAVIIAIPHFMV | 165 |
| VHL/E | 166 | VTKKDNQCMTDYDYLEVSYPIILNVELMLGAFV | 198 |
| VHL/E | 199 | IPLSVISYCYYRISRIVAVSQSRHKGRIVRVLI | 231 |
| VHL/E | 232 | AVVLVFIIFWLPYHLTLFVDTLKLLKWISSSCE | 264 |
| VHL/E | 265 | FEKSLKRALILTESLAFCHCCLNPLLYVFVGTK | 297 |
| VHL/E | 298 | FRQELHCLLAEFRQRLFSRDVSWYHSMSFSRRS | 330 |
| VHL/E | 331 | SPSRRETSSDTLSDEACRVSQIIP | 354 |

FIG. 1B

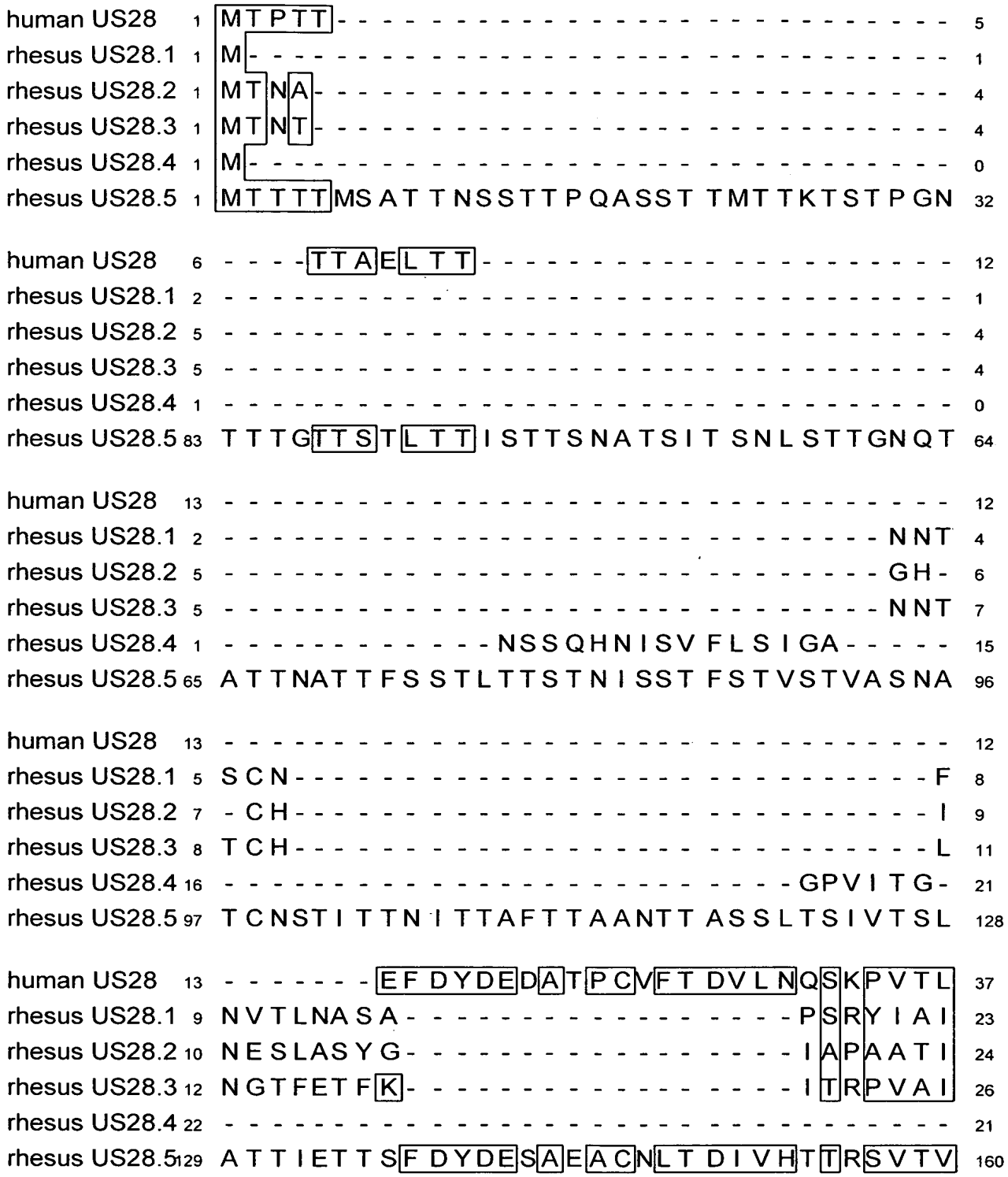


FIG. 2A

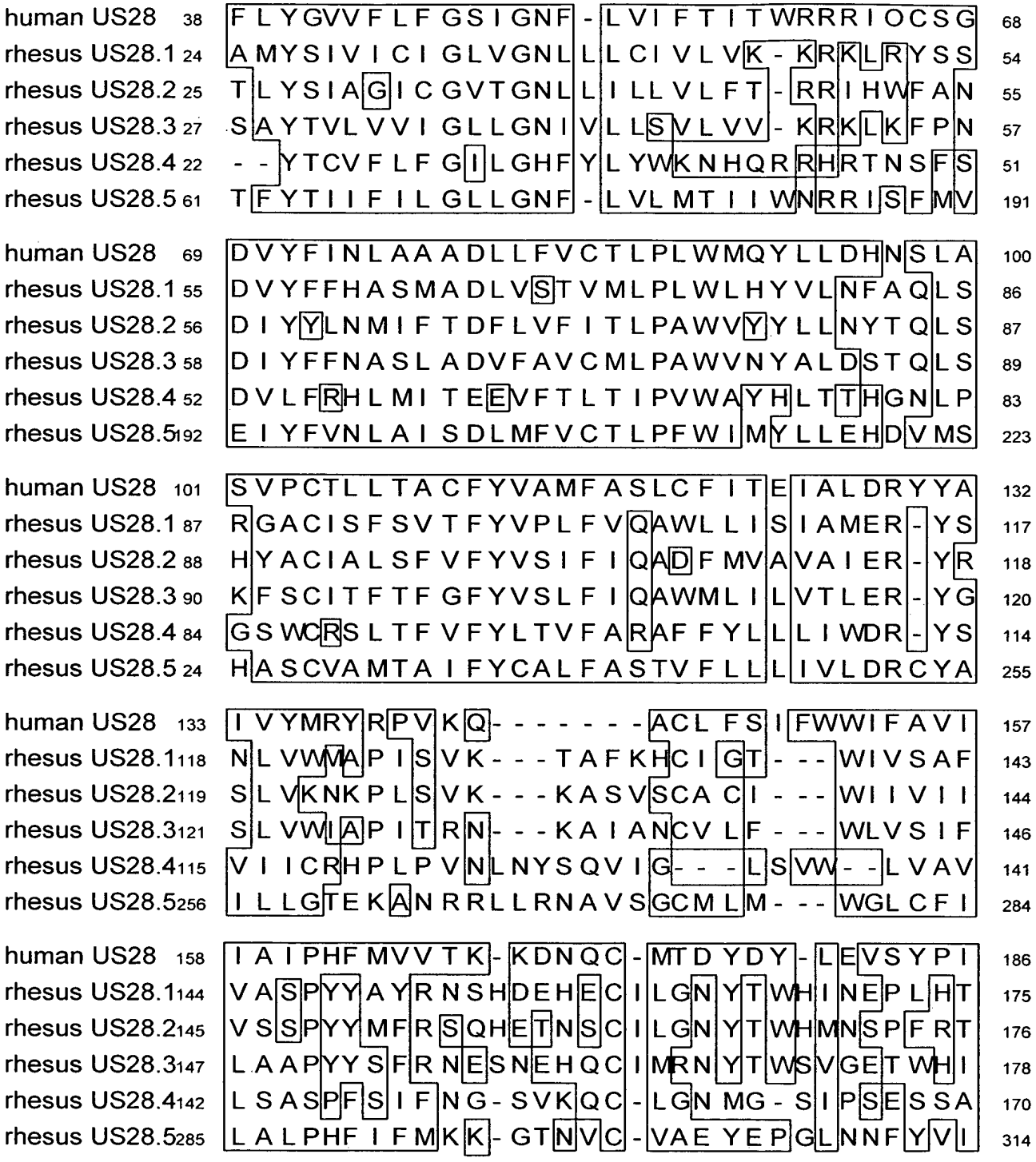


FIG. 2B

```
human US28  187 ILNVELMLGAFVIPLSVISYCYYRISRIVAVS 218
rhesus US28.1176 CMDVVIIVWTFLAPVLVTIIASVKM-RRTTWG 206
rhesus US28.2177 TMDASINIWSFVVPAVTTLLIARRIYV-CTSG 207
rhesus US28.3179 ALDFLITLITFIMPVTIVLALSFKMARWSTFG 210
rhesus US28.4171 VLNLEVHLCSFWLPLIMSANCYYQAKRRASPD 202
rhesus US28.5245 FINTEVNLCTLVLPAAAIIYWYLKLTKALKTH 346

human US28  219 QS-RHKGRIVRVLIAVVLVFIIFWLPYHLTLF 249
rhesus US28.1207 NT-RLNEKNSDILIVLVVMTVFFWGPFNIVLV 237
rhesus US28.2208 NK-KMNARASGLLEAMVISMLFFGGLFNLNIF 238
rhesus US28.3211 YR-NLTSRTSLILILILTVAAGFWGPFHLFMF 241
rhesus US28.4203 Q--LHELYRCSLLITIITTYAIVWFPFHLALL 232
rhesus US28.5347 ERLRHRLTSLNIVLAVVIVFALFWLPYNLMLM 378

human US28  250 VDTLKL-LKWISSSCEFERSLKRALILTESLA 280
rhesus US28.1238 IDNILQRYYDT-TNCDVEKIKHIMAMISEAIV 268
rhesus US28.2239 RD-IVSDTSEDNKDCTYLKQEHFIRMVGVALV 269
rhesus US28.3242 IENVAGQIYHIQKDCWYLQLRHLCSLMTETLV 273
rhesus US28.4233 IDALIS-ISHVEPSSALHWA--SIVVTCKSFT 261
rhesus US28.5379 MYSLVH-MQ-IPWECSSEKILRRSLIITESIA 408

human US28  281 FCHCCLNPLLYVFVGTKFRQELHCLLAEFRQR 312
rhesus US28.1269 YFRGITAPIIYVGISGRFREEIYSLFRRQPYN 300
rhesus US28.2270 YGRAIFNPFMYMCVSTRLRQEIKCLFMRIPYE 301
rhesus US28.3274 FLRSVFNPYIYMIISYKFRQQVRSLLKRTQYD 305
rhesus US28.4262 FVYAGISPLVYFTCCPTVRRELLMSLRPFFT- 292
rhesus US28.5409 LSHCCINPIIYLLFGPRCRSEFCHLLRCCFTR 440

human US28  313 LFSRDVSW--YHSMSFSRRSSPSRRETSSDTL 342
rhesus US28.1301 DLDPDAN-----QFMIELTSQGRSRNRNARQS 327
rhesus US28.2302 TLDAEHA-----KLMVNLKNRNANVPDPK--- 325
rhesus US28.3306 ALDTTQL-----AETMQLKAKGVPVSDPA--- 329
rhesus US28.4293 -------WISSKTRRGYAPIKTQPLNIPDEPI 317
rhesus US28.5441 L-CPHRSWSSIRAETVSISLSHSQVSASSEDD 471

human US28  343 SDEVCRVSQIIP 354
rhesus US28.1328 ESNVPQPEECFW 339
rhesus US28.2326 ----PREYESVL 333
rhesus US28.3380 ----PHDCECFL 337
rhesus US28.4318 DNKSPHLLN--E 327
rhesus US28.5472 DNDVHDELQFLI 483
```

FIG. 2C

```
human UL78   1 MSPSVEETTSVTESIMFAIVSFKHMGPFEGY  31
rhesus UL78  1 -----------------------------  0

human UL78  32 SMSADRAASDLLIGMFGSVSLVNLLTLIGCL  62
rhesus UL78  1 -MITERVLAGILAGMTAAGSLVILLAVV--M  28

human UL78  63 WVLRVTRP--PVSVMIFTWNLVLSQFFSILA  91
rhesus UL78 29 WLNMLDRAGMPMAVGHYTGNLVLTQVICIFS  59

human UL78  92 TMLSKGIMLRGALNLSLCRLVLFVDDVGLYS 122
rhesus UL78 60 -MLASKIVGMTSAANMGFCGIVVFLEDTGLY  89

human UL78 123 TALFFLFLILDRLSAISYGRDLWHHE-TRFN 152
rhesus UL78 90 VTSLLFMFMILDRMAAFLNGRLFWRQQTTKQ 120

human UL78 153 AGVALYAVAFAWVLSIVAAVPTAATGSLDYR 183
rhesus UL78 121 NLSTSVYIILFCWVLGMAAAVPSAAVAAPNS 151

human UL78 184 WLGCQIPIQYAAVDLTIKMWFLLGAPMIAVL 214
rhesus UL78 152 RWERCEIPVSYAAIDMIVKLWFVLLAPVVLI 182

human UL78 215 ANVVELAYSDRRDHVWSYVGRVCTFYVTCLM 245
rhesus UL78 183 MAVIIQSSYHRDRERIWYYARRVFMFYTACF 213

human UL78 246 LFVPYYCFRV------LRGV-LQPASAAGTG 269
rhesus UL78 214 VMMVPYYFVRVMLSDFALVDIKTKTANSDGC 244

human UL78 270 FGIMDYVELATRTLLTMRLGILPLFIIAFFS 300
rhesus UL78 245 DSTFLDYLNMFTHVIYSFKLVVFALFIVLFC 275

human UL78 301 REPTKDLDDSFDYLVERCQQSCHGHFVRRLV 331
rhesus UL78 276 SINPMETLEECLERADAERQSRSEASQGERR 306

human UL78 332 QALKRAMYSVELAVCYFSTSVRDVAEAVKKS 362
rhesus UL78 307 LPINTCCIKLIELIKQYVSTLSKATRDNSGE 337

human UL78 363 SSRCYADATSAAVVVTTTTSEKATLVEHAEG 393
rhesus UL78 338 RANLPENAEDIGTTGSDQLPTEVTVTPNSSA 368

human UL78 394 MASEMCPGTTIDVSAESSSVLCTDGENTVAS 424
rhesus UL78 369 VFSTGGTVSPV                   379

                                              431
human UL78 425 DATVTAL
```

FIG. 3

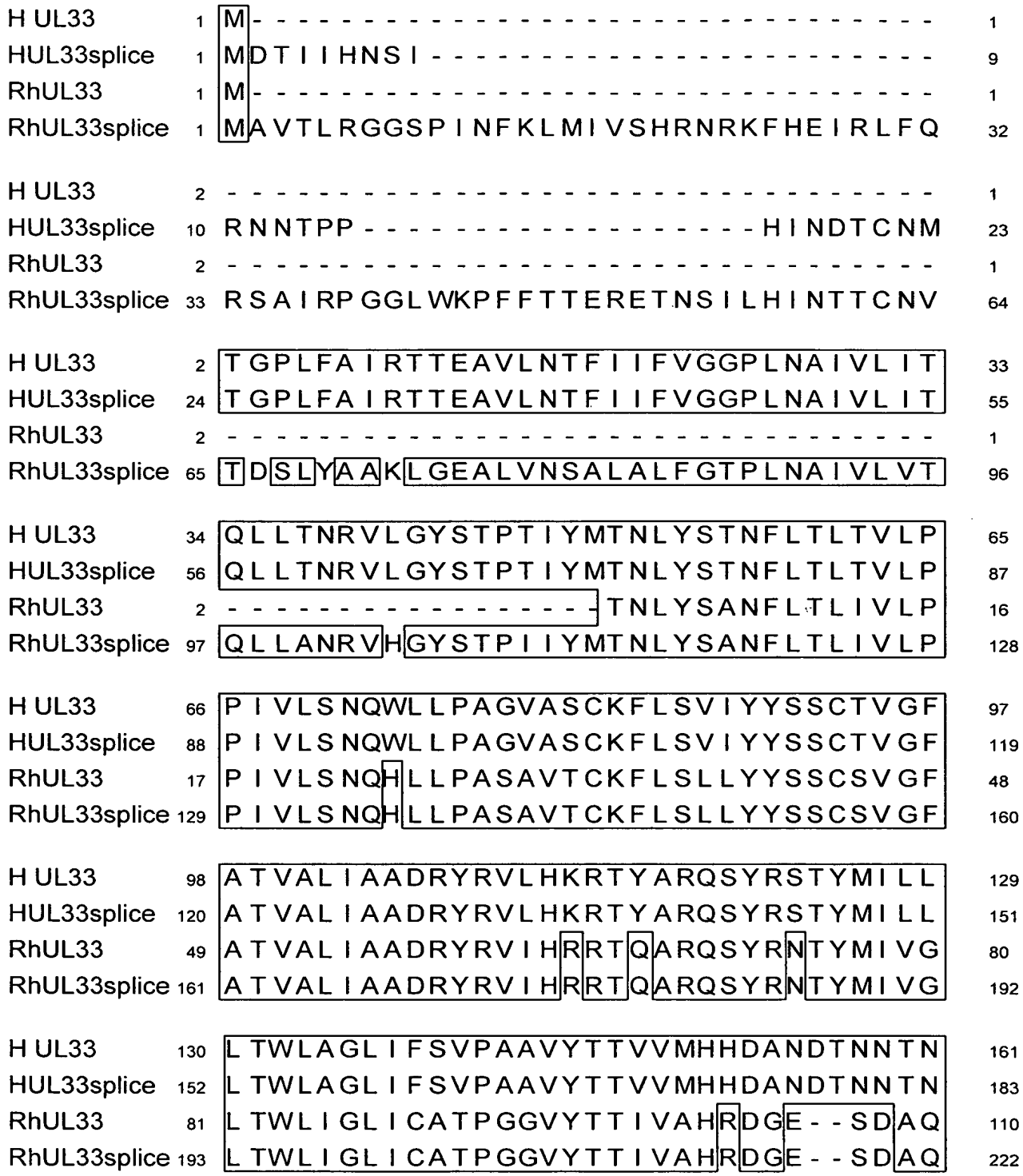


FIG. 4A

```
H UL33          162 GHATCVLYFVAEEVHTVLLSWKVLLTMVWGAA 193
HUL33splice     184 GHATCVLYFVAEEVHTVLLSWKVLLTMVWGAA 215
RhUL33          111 RHNTCIMHFAYDEVY-VLMVWKLLIVLVWGIV 141
RhUL33splice    223 RHNTCIMHFAYDEVY-VLMVWKLLIVLVWGIV 253

H UL33          194 PVIMMTWFYAFFYSTVQRTSLKQRSRTLTFVS 225
HUL33splice     216 PVIMMTWFYAFFYSTVQRTSLKQRSRTLTFVS 247
RhUL33          142 PVVMMSWFYAFFYNTVQRTAKKQQ-RTLKFVK 172
RhUL33splice    254 PVVMMSWFYAFFYNTVQRTAKKQQ-RTLKFVK 284

H UL33          226 VLLISFVALQTPYVSLMIFNSYATTAWPMQCE 257
HUL33splice     248 VLLISFVALQTPYVSLMIFNSYATTAWPMQCE 279
RhUL33          173 VLLLSFIIIQTPYVSIMIFNTYATVGWPMECA 204
RhUL33splice    285 VLLLSFIIIQTPYVSIMIFNTYATVGWPMECA 316

H UL33          258 HLTLRRTIGTLARVVPHLHCLINPILYALLGH 289
HUL33splice     280 HLTLRRTIGTLARVVPHLHCLINPILYALLGH 311
RhUL33          205 DLTRRRVINTFSRLVPNLHCMVNPILYALMGN 236
RhUL33splice    317 DLTRRRVINTFSRLVPNLHCMVNPILYALMGN 348

H UL33          290 DFLQRMRQCFRGQLLDRRAFLRSQNNQRATAE 321
HUL33splice     312 DFLQRMRQCFRGQLLDRRAFLRSQNNQRATAE 343
RhUL33          237 DFVSKVGQCFRGELTNRRTFLRSKQQARNSDD 258
RhUL33splice    349 DFVSKVGQCFRGELTNRRTFLRSKQQARNSDD 380

H UL33          322 TNLAAGNNSQSVATSLDTNSKNYNQHAKRSVS 353
HUL33splice     344 TNLAAGNNSQSVATSLDTNSKNYNQHAKRSVS 375
RhUL33          269 VPTIVSQQP-ATPTIVNKPEK--NPHVKRGVS 297
RhUL33splice    381 VPTIVSQQP-ATPTIVNKPEK--NPHVKRGVS 409

H UL33          354 FNFPSGTWKGGQKTASNDTSTKIPHRLSQSHH 385
HUL33splice     376 FNFPSGTWKGGQKTASNDTSTKIPHRLSQSHH 407
RhUL33          298 FSVSASSELAAAKKAKDKA-----KRLSMSHQ 324
RhUL33splice    410 FSVSASSELAAAKKAKDKA-----KRLSMSHQ 436

H UL33          386 NLSGV 390
HUL33splice     408 NLSGV 412
RhUL33          325 NLRLT 329
RhUL33splice    437 NLRLT 441
```

FIG. 4B

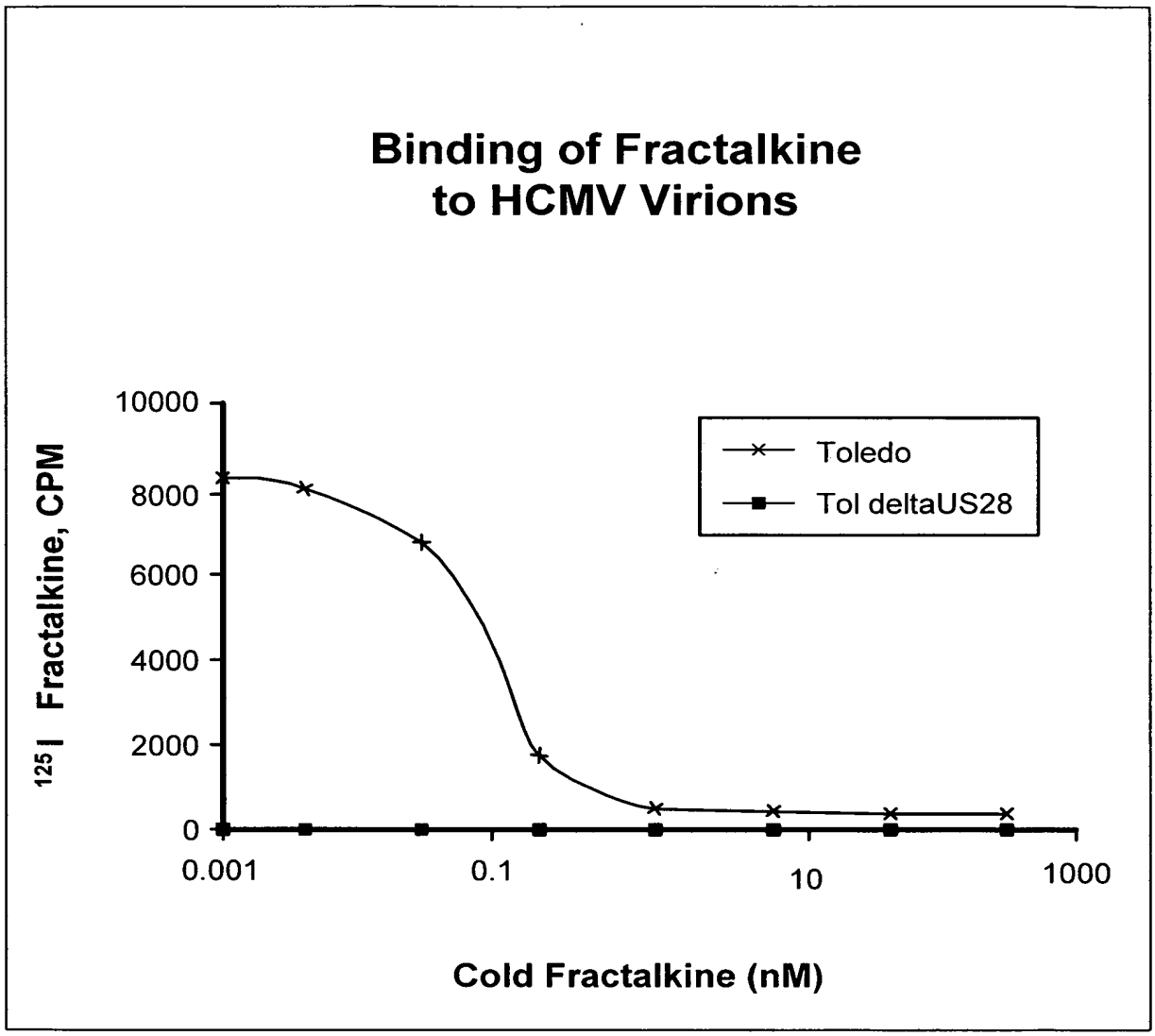


FIG. 5

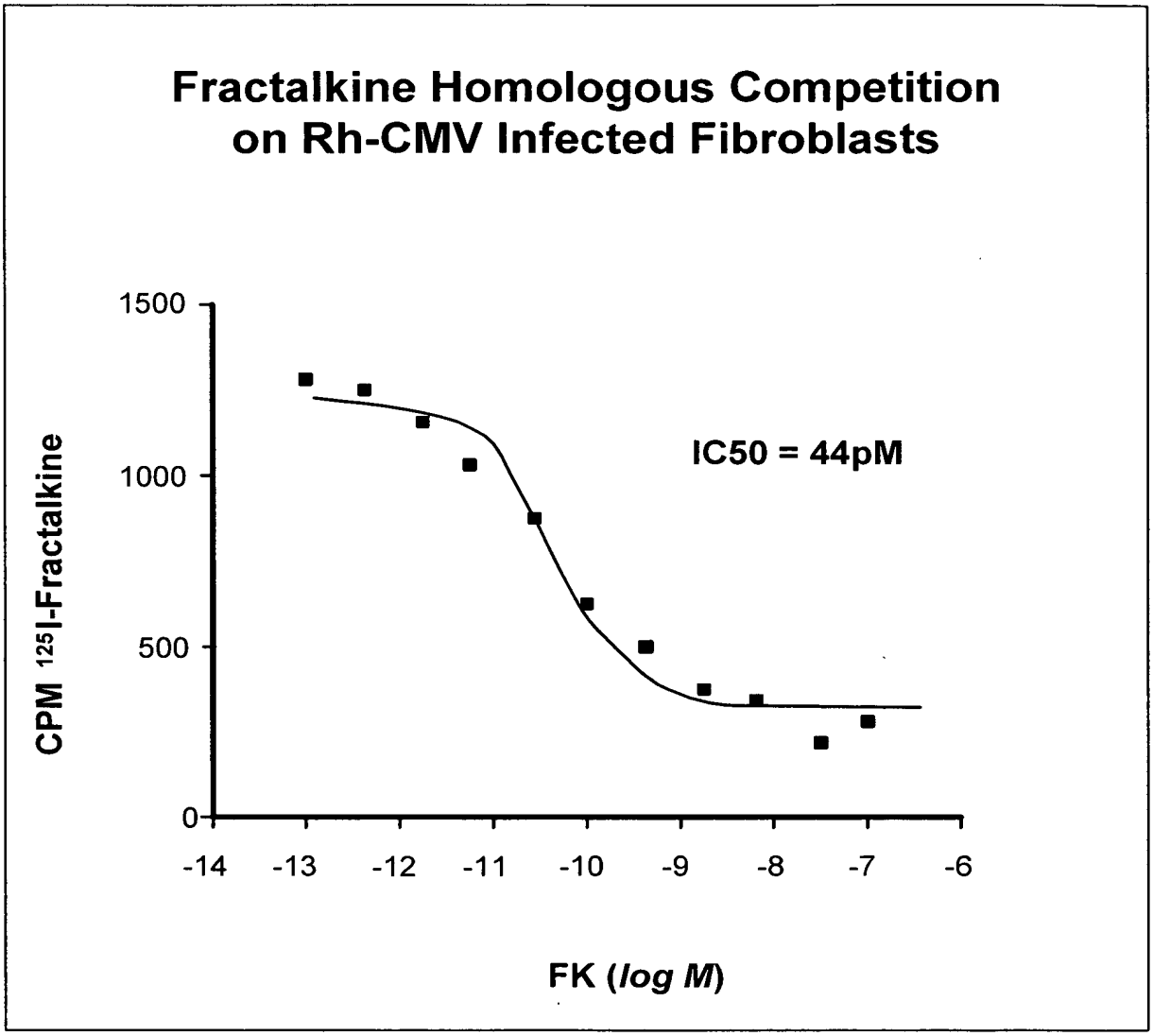


FIG. 6

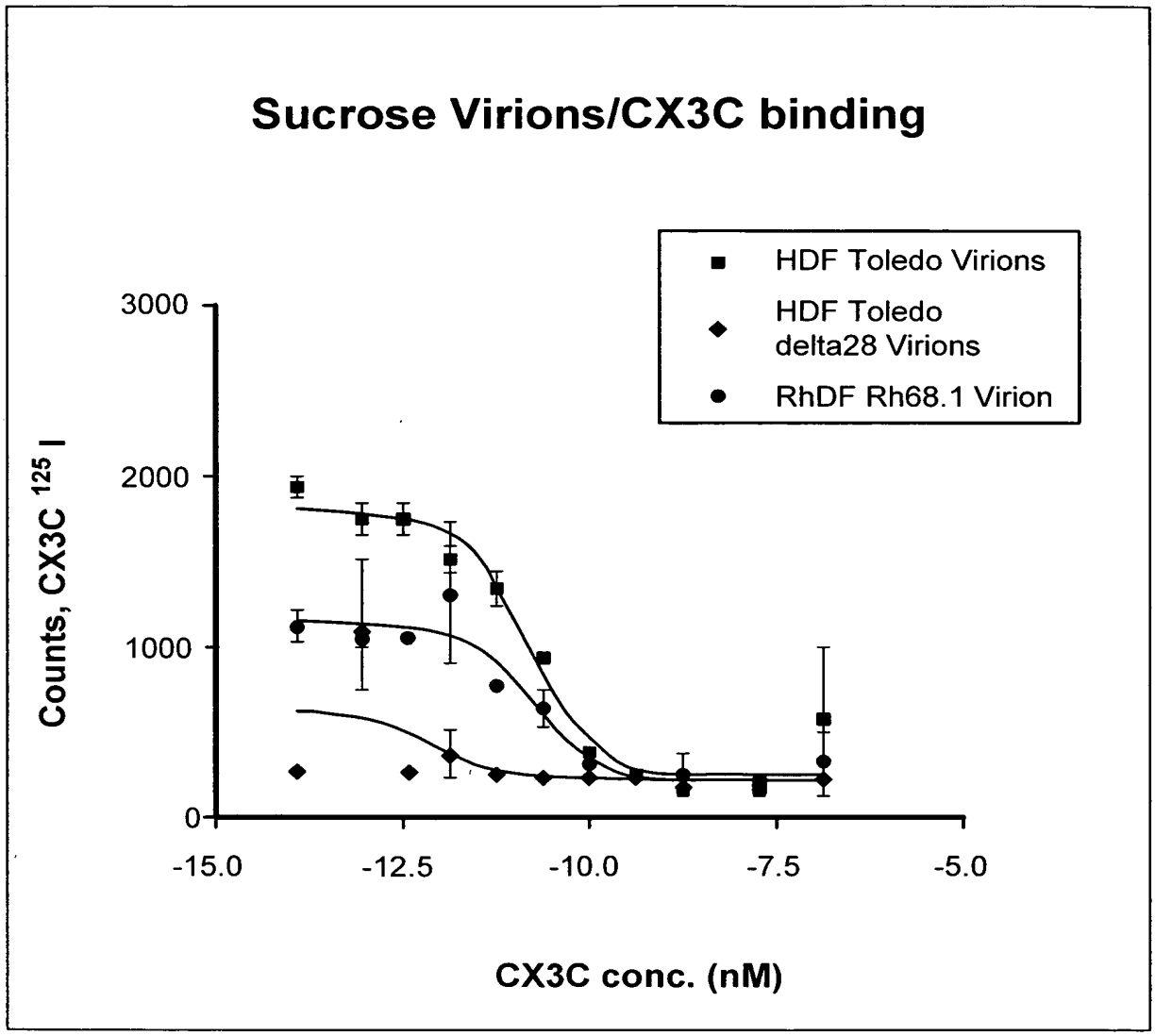


FIG. 7